

## SEQUENCE LISTING

<110> Yumi Matsuzaki  
 Eiichiro Kimura  
 Tsuyoshi Nakamatsu  
 Osamu Kurahashi  
 Yoshio Kawahara  
 Shinichi Sugimoto

<120> Plasmid Autonomously Replicable in Coryneform Bacteria

<130>

<150> JP 11-228391

<151> 1999-08-12

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 1479

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(1476)

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Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser	
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Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp	
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cgc agc atg ttt cac ggg tgc ccc acc cgg gat ttc tcc gcg gcc tgg	192
Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp	
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gtc aaa gac ccg gaa acc gga gaa acc cgc ccc aag ctg cac aga gtt	240
Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val	
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ggc acc cgc tca ctt tcc cgg tgc cag tac gtt gcc ctg acc cac ccg	288
Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro	
85 90 95	
cag cgc tcc gcg gtg ctg gtc tta gac atc gac atc ccc agc cac cag	336
Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln	
100 105 110	
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Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu	
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Cancelled by amdt a

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	Ala	Ala	Glu	Gly	Thr	Thr	Ser	Ser	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Thr	
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	Thr	Glu	Glu	Met	Thr	Arg	Val	Phe	Gly	Ala	Asp	Gln	Ala	Phe	Ser	His	
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	Arg	Leu	Ser	Arg	Trp	Pro	Leu	His	Val	Ser	Asp	Asp	Pro	Thr	Ala	Tyr	
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	Ser	Trp	His	Cys	Gln	His	Asn	Arg	Val	Asp	Ile	Leu	Asp	Glu	Leu	Met	
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	Glu	Val	Ala	Arg	Thr	Met	Thr	Gly	Ser	Lys	Lys	Pro	Arg	Glu	His	Ala	
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	His	Gln	Glu	Phe	Ser	Ser	Gly	Arg	Ala	Arg	Ile	Glu	Ala	Ala	Arg	Lys	
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	Ala	Thr	Ala	Glu	Ala	Lys	Ala	Leu	Ala	Ala	Leu	Asp	Ala	Thr	Leu	Pro	
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	Thr	Ala	Leu	Glu	Ala	Ser	Gly	Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Leu	
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	Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His	
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	Ala	Leu	Thr	Val	Gly	Tyr	Gln	Leu	Lys	Ala	Ala	Gly	Glu	Arg	Leu	Lys	
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	Asp	Ala	Lys	Ile	Ile	Asp	Ala	Tyr	Glu	Arg	Ala	Tyr	Asn	Val	Ala	Gln	
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	Arg	Gln	Thr	Met	Ala	Arg	Arg	Val	Arg	Ala	Tyr	Val	Ala	Lys	Gly	Gln	
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	Pro	Thr	Val	Ser	Ala	Arg	Ser	Thr	Gln	Thr	Gln	Ser	Ser	Arg	Gly	Arg	
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	Lys	Ala	Leu	Ala	Thr	Met	Gly	Arg	Arg	Gly	Gly	Gln	Lys	Ala	Ala	Glu	
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Ala	Ser	Thr	Asn	Ser	Gly	Tyr	Gly	Phe	Arg	His	Val	Trp	Ala	Ser	Leu		
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gaa	aaa	tgc	cta	cgc	gac	gag	caa	atc	atg	gaa	gaa	aca	ggg	ctt	tca	1392	
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Arg	Ala	Thr	Val	Thr	Arg	His	Trp	Val	His	Cys	Glu	Arg	Leu	Ala	Cys		
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&lt;210&gt; 2

&lt;211&gt; 492

&lt;212&gt; PRT

<213> *Corynebacterium thermoaminogenes*

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Arg	Ser	Met	Phe	His	Gly	Cys	Pro	Thr	Arg	Asp	Phe	Ser	Ala	Ala	Trp		
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Val	Lys	Asp	Pro	Glu	Thr	Gly	Glu	Thr	Arg	Pro	Lys	Leu	His	Arg	Val		
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			165					170					175				
Thr	Glu	Glu	Met	Thr	Arg	Val	Phe	Gly	Ala	Asp	Gln	Ala	Phe	Ser	His		
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Thr	Ala	Leu	Glu	Ala	Ser	Gly	Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Leu		
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Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His		
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 Ala Val Gly Ala Asp Gly Arg Glu Pro Asp Leu Pro Ala Met Arg Asp  
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 Arg Gln Thr Met Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln  
 355 360 365  
 Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg  
 370 375 380  
 Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu  
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 Arg Trp Lys Thr Asp Pro Asn Gly Lys Tyr Ala Gln Glu Asn Arg Gln  
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 420 425 430  
 Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu  
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 Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser  
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&lt;210&gt; 3

&lt;211&gt; 1479

&lt;212&gt; DNA

<213> *Corynebacterium thermoaminogenes*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1476)

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tac tcc act gat ctg ttc gac acc cac cct gag ctg gct tta cgc tcc	96
Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser	
20 25 30	
cgg ggt tgg aat cac cag gac gcc gca gag ttc ctg gcc cac ctg gat	144
Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp	
35 40 45	
cgc agc atg ttt cac ggg tgc ccc acc cgg gat ttc tcc gcg gcc tgg	192
Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp	
50 55 60	
gtc aaa gac ccg gaa acc gga gaa acc cgc ccc aag ctg cac aga gtt	240
Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val	
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ggc acc cgc tca ctt tcc cgg tgc cag tac gtt gcc ctg acc cac ccg	288
Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro	
85 90 95	
cag cgc tcc gcg gtg ctg gtc tta gac atc gac atc ccc agc cac cag	336
Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln	
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Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn	
130 135 140	
ccg ttg tcg gga aag tgc cag ctc atc tgg tgc att gac ccg gtg ttc	480
Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe	
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165 170 175	
acc gag gaa atg acc cgt gtg ttc ggc gct gac cag gca ttt tcc cac	576
Thr Glu Glu Met Thr Arg Val Phe Gly Ala Asp Gln Ala Phe Ser His	
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Arg Leu Ser Arg Trp Pro Leu His Val Phe Asp Asp Pro Thr Ala Tyr	
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tcc tgg cac tgc cag cac aac cga gtc gat att ctt gat gag ctg atg	672
Ser Trp His Cys Gln His Asn Arg Val Asp Ile Leu Asp Glu Leu Met	
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gag gta gcc cgc acg atg acc gga tca aaa aag ccg aga aag cac gct	720
Glu Val Ala Arg Thr Met Thr Gly Ser Lys Lys Pro Arg Lys His Ala	
225 230 235 240	
cac cag gag ttt tcc agc ggt cgg gca cgg atc gaa gcc gcg cgg aaa	768
His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys	
245 250 255	
gcc acc gca gag gcc aaa gcg ctt gcc gcc ttg gac gcc acg ctg cct	816
Ala Thr Ala Glu Ala Lys Ala Leu Ala Ala Leu Asp Ala Thr Leu Pro	
260 265 270	
acg gcg ctg gag gca tca ggc gat ctc att gac ggg gtg cgg gtg ttg	864
Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu	
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Trp Ala Ala Glu Gly Arg Ala Ala Arg Asp Glu Thr Ala Phe Arg His	
290 295 300	
gcg ttg acc gtg ggt tat cag ctt aaa gcc gca ggt gaa cgc ctg aaa	960
Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys	
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Asp Ala Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln	
325 330 335	
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Ala Val Gly Ala Asp Gly Arg Glu Pro Asp Leu Pro Ala Met Arg Asp	
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Arg Gln Thr Met Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln	
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ccc acg gtc agc gcc agg agc aca cag acc cag agc agt cgg ggc cgg	1152
Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg	
370 375 380	
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Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu	
385 390 395 400	
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Arg Trp Lys Thr Asp Pro Asn Gly Lys Tyr Ala Gln Glu Asn Arg Gln	

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gcg agc acg aat tct ggc tac ggt ttc cga cac gta tgg gcc agc ttg						1344
Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu						
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gaa aaa tgc cta cgc gac gag caa atc atg gaa gaa aca ggg ctt tca						1392
Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser						
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cga gct acc gtg acg cgc cat tgg gtg cac tgc gag agg ctg gcc tgc						1440
Arg Ala Thr Val Thr Arg His Trp Val His Cys Glu Arg Leu Ala Cys						
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tgc caa atc ctt agg ggg gct cac gcc gta cac aga taa						1479
Cys Gln Ile Leu Arg Gly Ala His Ala Val His Arg						
	485		490			

&lt;210&gt; 4

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium thermoaminogenes

&lt;400&gt; 4

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Arg	Gly	Trp	Asn	His	Gln	Asp	Ala	Ala	Glu	Phe	Leu	Ala	His	Leu	Asp
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Val	Lys	Asp	Pro	Glu	Thr	Gly	Glu	Thr	Arg	Pro	Lys	Leu	His	Arg	Val
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			85						90					95	
Gln	Arg	Ser	Ala	Val	Leu	Val	Leu	Asp	Ile	Asp	Ile	Pro	Ser	His	Gln
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Ala	Gly	Gly	Asn	Ile	Glu	His	Leu	His	Pro	Gln	Val	Tyr	Ala	Thr	Leu
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Glu	Arg	Trp	Ala	Arg	Val	Glu	Lys	Ala	Pro	Ala	Trp	Ile	Gly	Val	Asn
	130					135					140				
Pro	Leu	Ser	Gly	Lys	Cys	Gln	Leu	Ile	Trp	Cys	Ile	Asp	Pro	Val	Phe
	145				150					155				160	
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			165					170					175		
Thr	Glu	Glu	Met	Thr	Arg	Val	Phe	Gly	Ala	Asp	Gln	Ala	Phe	Ser	His
		180						185					190		
Arg	Leu	Ser	Arg	Trp	Pro	Leu	His	Val	Phe	Asp	Asp	Pro	Thr	Ala	Tyr
		195				200						205			
Ser	Trp	His	Cys	Gln	His	Asn	Arg	Val	Asp	Ile	Leu	Asp	Glu	Leu	Met
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Glu	Val	Ala	Arg	Thr	Met	Thr	Gly	Ser	Lys	Lys	Pro	Arg	Lys	His	Ala
	225				230					235				240	
His	Gln	Glu	Phe	Ser	Ser	Gly	Arg	Ala	Arg	Ile	Glu	Ala	Ala	Arg	Lys
			245					250					255		
Ala	Thr	Ala	Glu	Ala	Lys	Ala	Leu	Ala	Ala	Leu	Asp	Ala	Thr	Leu	Pro

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 Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu  
 275 280 285  
 Trp Ala Ala Glu Gly Arg Ala Ala Arg Asp Glu Thr Ala Phe Arg His  
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 Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys  
 305 310 315 320  
 Asp Ala Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln  
 325 330 335  
 Ala Val Gly Ala Asp Gly Arg Glu Pro Asp Leu Pro Ala Met Arg Asp  
 340 345 350  
 Arg Gln Thr Met Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln  
 355 360 365  
 Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg  
 370 375 380  
 Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu  
 385 390 395 400  
 Arg Trp Lys Thr Asp Pro Asn Gly Lys Tyr Ala Gln Glu Asn Arg Gln  
 405 410 415  
 Arg Leu Glu Ala Ala Asn Lys Arg Arg Gln Val Ser Trp Asn Lys Tyr  
 420 425 430  
 Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu  
 435 440 445  
 Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser  
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 465 470 475 480  
 Cys Gln Ile Leu Arg Gly Ala His Ala Val His Arg  
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<210> 5  
 <211> 1479  
 <212> DNA  
 <213> *Corynebacterium thermoaminogenes*

<220>  
 <221> CDS  
 <222> (1)..(1476)

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 Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser  
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 Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp  
 35 40 45  
 cgc agc atg ttt cac ggg tgc ccc acc cgg gat ttc tcc gcg gcc tgg 192  
 Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp  
 50 55 60  
 gtc aaa gac ccg gaa acc gga gaa acc cgc ccc aag ctg cac aga gtt 240  
 Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val  
 65 70 75 80  
 ggc acc cgc tca ctt tcc cgg tgc cag tac gtt gcc ctg acc cac ccg 288

Gly	Thr	Arg	Ser	Leu	Ser	Arg	Cys	Gln	Tyr	Val	Ala	Leu	Thr	His	Pro	
				85					90					95		
cag	cgc	tcc	gcg	gtg	ctg	gtc	tta	gac	atc	gac	atc	ccc	agc	cac	cag	336
Gln	Arg	Ser	Ala	Val	Leu	Val	Leu	Asp	Ile	Asp	Ile	Pro	Ser	His	Gln	
			100					105					110			
gcc	ggc	ggg	aac	atc	gag	cac	ctt	cac	ccg	cag	gta	tac	gcc	acc	ttg	384
Ala	Gly	Gly	Asn	Ile	Glu	His	Leu	His	Pro	Gln	Val	Tyr	Ala	Thr	Leu	
			115				120					125				
gag	cgt	tgg	gca	cgg	gtg	gag	aaa	gcg	ccg	gcc	tgg	atc	ggg	gtg	aac	432
Glu	Arg	Trp	Ala	Arg	Val	Glu	Lys	Ala	Pro	Ala	Trp	Ile	Gly	Val	Asn	
			130			135					140					
ccg	ttg	tgc	gga	aag	tgc	cag	ctc	atc	tgg	tgc	att	gac	ccg	gtg	ttc	480
Pro	Leu	Ser	Gly	Lys	Cys	Gln	Leu	Ile	Trp	Cys	Ile	Asp	Pro	Val	Phe	
				150						155					160	
gcc	gcc	gag	ggc	acc	acc	agc	tgc	aac	acc	cgc	ctg	cta	gcg	gcc	acc	528
Ala	Ala	Glu	Gly	Thr	Ser	Ser	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Thr		
				165				170						175		
acc	gag	gaa	atg	acc	cgt	gtg	ttc	ggc	gct	gac	cag	gca	ttt	tcc	cac	576
Thr	Glu	Glu	Met	Thr	Arg	Val	Phe	Gly	Ala	Asp	Gln	Ala	Phe	Ser	His	
			180				185						190			
cgg	ctg	agc	cgg	tgg	ccg	ctg	cat	gtt	tct	gat	gat	ccg	acc	gcg	tac	624
Arg	Leu	Ser	Arg	Trp	Pro	Leu	His	Val	Ser	Asp	Asp	Pro	Thr	Ala	Tyr	
			195			200						205				
tcc	tgg	cac	tgc	cag	cac	aac	cga	gtc	gat	acg	ctt	gat	gag	ctg	atg	672
Ser	Trp	His	Cys	Gln	His	Asn	Arg	Val	Asp	Thr	Leu	Asp	Glu	Leu	Met	
			210			215					220					
gag	gta	gcc	cgc	acg	atg	acc	gga	tca	aaa	aag	ccg	aga	aag	cac	gct	720
Glu	Val	Ala	Arg	Thr	Met	Thr	Gly	Ser	Lys	Lys	Pro	Arg	Lys	His	Ala	
				230					235						240	
cac	cag	gag	ttt	tcc	agc	ggc	cgg	gca	cgg	atc	gaa	gcc	gcg	cgg	aaa	768
His	Gln	Glu	Phe	Ser	Gly	Arg	Ala	Arg	Ile	Glu	Ala	Ala	Arg	Lys		
				245				250					255			
gcc	acc	gca	gag	gcc	aaa	gcg	ctt	gcc	gtg	gac	gcc	acg	ctg	cct		816
Ala	Thr	Ala	Glu	Ala	Lys	Ala	Leu	Ala	Ala	Leu	Asp	Ala	Thr	Leu	Pro	
				260			265					270				
acg	gcg	ctg	gag	gca	tca	ggc	gat	ctc	att	gac	ggg	gtg	cgg	gtg	ttg	864
Thr	Ala	Leu	Glu	Ala	Ser	Gly	Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Leu	
				275			280					285				
tgg	gca	gca	gag	ggg	cgt	gca	gcc	cgt	gat	gag	aca	gcg	ttt	cgc	cat	912
Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His	
				290		295				300						
gcg	ttg	acc	gtg	ggt	tat	cag	ctt	aaa	gcc	gca	ggt	gaa	cgc	ctg	aaa	960
Ala	Leu	Thr	Val	Gly	Tyr	Gln	Leu	Lys	Ala	Ala	Gly	Glu	Arg	Leu	Lys	
				310					315					320		
gat	gcc	aag	atc	att	gat	gcg	tat	gag	cgt	gcc	tac	aac	gtc	gcc	cag	1008
Asp	Ala	Lys	Ile	Ile	Asp	Ala	Tyr	Glu	Arg	Ala	Tyr	Asn	Val	Ala	Gln	
				325				330					335			
gcg	gtg	gga	gct	gat	ggg	cgt	gaa	ccg	gat	ctg	cct	gcc	atg	cgt	gat	1056
Ala	Val	Gly	Ala	Asp	Gly	Arg	Glu	Pro	Asp	Leu	Pro	Ala	Met	Arg	Asp	
				340			345					350				
cgt	cag	acg	atg	gcc	cgc	cgt	gtg	cgc	gcc	tac	gtc	gcc	aaa	ggc	cag	1104
Arg	Gln	Thr	Met	Ala	Arg	Arg	Val	Arg	Ala	Tyr	Val	Ala	Lys	Gly	Gln	
				355			360					365				
ccc	acg	gtc	agc	gcc	agg	agc	aca	cag	acc	cag	agc	agt	cgg	ggc	cgg	1152
Pro	Thr	Val	Ser	Ala	Arg	Ser	Thr	Gln	Thr	Gln	Ser	Ser	Arg	Gly	Arg	
				370			375				380					

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aaa gcc ctg gcc acc atg ggc cgc aga ggc ggg caa aaa gcc gct gaa 1200  
 Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu  
 385 390 395 400  
 cgc tgg aaa acc gat cct aac ggc aaa tac gcc caa gaa aac cgc caa 1248  
 Arg Trp Lys Thr Asp Pro Asn Gly Lys Tyr Ala Gln Glu Asn Arg Gln  
 405 410 415  
 cga ctc gaa gct gca aac aag cga cgt caa gtc agc tgg aac aaa tac 1296  
 Arg Leu Glu Ala Ala Asn Lys Arg Arg Gln Val Ser Trp Asn Lys Tyr  
 420 425 430  
 gcg agc acg aat tct ggc tac ggt ttc cga cac gta tgg gcc agc ttg 1344  
 Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu  
 435 440 445  
 gaa aaa tgc cta cgc gac gag caa atc atg gaa gaa aca ggg ctt tca 1392  
 Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser  
 450 455 460  
 cga gct acc gtg acg cgc cat tgg gtg cac tgc gag agg ctg gcc tgc 1440  
 Arg Ala Thr Val Thr Arg His Trp Val His Cys Glu Arg Leu Ala Cys  
 465 470 475 480  
 tgc caa atc ctt agg ggg gct cac gcc gta cac aga taa 1479  
 Cys Gln Ile Leu Arg Gly Ala His Ala Val His Arg  
 485 490

&lt;210&gt; 6

&lt;211&gt; 492

&lt;212&gt; PRT

<213> *Corynebacterium thermoaminogenes*

&lt;400&gt; 6

Met Thr Leu Ala Asp Ser Pro Gly Thr Tyr Thr Ala Asp Ala Trp Asn  
 1 5 10 15  
 Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser  
 20 25 30  
 Arg Gly Trp Asn His Gln Asp Ala Glu Phe Leu Ala His Leu Asp  
 35 40 45  
 Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp  
 50 55 60  
 Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val  
 65 70 75 80  
 Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro  
 85 90 95  
 Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln  
 100 105 110  
 Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu  
 115 120 125  
 Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn  
 130 135 140  
 Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe  
 145 150 155 160  
 Ala Ala Glu Gly Thr Ser Ser Asn Thr Arg Leu Leu Ala Ala Thr  
 165 170 175  
 Thr Glu Glu Met Thr Arg Val Phe Gly Ala Asp Gln Ala Phe Ser His  
 180 185 190  
 Arg Leu Ser Arg Trp Pro Leu His Val Ser Asp Asp Pro Thr Ala Tyr  
 195 200 205  
 Ser Trp His Cys Gln His Asn Arg Val Asp Thr Leu Asp Glu Leu Met  
 210 215 220

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Glu Val Ala Arg Thr Met Thr Gly Ser Lys Lys Pro Arg Lys His Ala  
 225 230 235 240  
 His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys  
 245 250 255  
 Ala Thr Ala Glu Ala Lys Ala Leu Ala Ala Leu Asp Ala Thr Leu Pro  
 260 265 270  
 Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu  
 275 280 285  
 Trp Ala Ala Glu Gly Arg Ala Ala Arg Asp Glu Thr Ala Phe Arg His  
 290 295 300  
 Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys  
 305 310 315 320  
 Asp Ala Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln  
 325 330 335  
 Ala Val Gly Ala Asp Gly Arg Glu Pro Asp Leu Pro Ala Met Arg Asp  
 340 345 350  
 Arg Gln Thr Met Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln  
 355 360 365  
 Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg  
 370 375 380  
 Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu  
 385 390 395 400  
 Arg Trp Lys Thr Asp Pro Asn Gly Lys Tyr Ala Gln Glu Asn Arg Gln  
 405 410 415  
 Arg Leu Glu Ala Ala Asn Lys Arg Arg Gln Val Ser Trp Asn Lys Tyr  
 420 425 430  
 Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu  
 435 440 445  
 Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser  
 450 455 460  
 Arg Ala Thr Val Thr Arg His Trp Val His Cys Glu Arg Leu Ala Cys  
 465 470 475 480  
 Cys Gln Ile Leu Arg Gly Ala His Ala Val His Arg  
 485 490

<210> 7  
 <211> 1377  
 <212> DNA  
 <213> *Corynebacterium thermoaminogenes*

<220>  
 <221> CDS  
 <222> (1)..(1374)

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 Met Thr Leu Ala Asp Ser Pro Gly Thr Tyr Thr Ala Asp Ala Trp Asn  
 1 5 10 15  
 tac tcc aca gat ctg ttc gac acc cac cct gag ctg gct tta cgc tcc 96  
 Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser  
 20 25 30  
 cgg ggt tgg aat cac cag gac gcc gcc gag ttc ctg gcc cac ctg gat 144  
 Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp  
 35 40 45  
 cgc agc atg ttt cac ggg tgc ccc acc cgg gat ttc tcc gcg gcc tgg 192  
 Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp

	50					55					60					
gtc	aaa	gac	ccg	gag	acc	gga	acc	cgc	cct	aag	ctg	cac	aga	gtc	240	
Val	Lys	Asp	Pro	Glu	Thr	Gly	Glu	Thr	Arg	Lys	Leu	His	Arg	Val		
65					70				75					80		
ggc	acc	cgg	tcg	ctt	tcc	cga	tgc	cag	tac	gtc	gcg	ctg	acc	cac	ccg	288
Gly	Thr	Arg	Ser	Leu	Ser	Arg	Cys	Gln	Tyr	Val	Ala	Leu	Thr	His	Pro	
				85					90					95		
cag	cgc	tcc	gcg	gtg	ctg	gtc	tta	gac	atc	gac	atc	ccc	agc	cac	cag	336
Gln	Arg	Ser	Ala	Val	Leu	Val	Leu	Asp	Ile	Asp	Ile	Pro	Ser	His	Gln	
			100					105					110			
gcc	ggc	ggg	aac	atc	gag	cac	ctt	cac	ccg	cag	gtc	tac	gcc	acc	ttg	384
Ala	Gly	Gly	Asn	Ile	Glu	His	Leu	His	Pro	Gln	Val	Tyr	Ala	Thr	Leu	
		115					120					125				
gag	cgc	tgg	gca	cgg	gtg	gag	aaa	gcg	ccg	gcc	tgg	atc	ggg	gtg	aac	432
Glu	Arg	Trp	Ala	Arg	Val	Glu	Lys	Ala	Pro	Ala	Trp	Ile	Gly	Val	Asn	
		130					135					140				
ccg	ttg	tca	gga	aag	tgc	cag	ctc	atc	tgg	tgc	att	gac	ccg	gtg	ttc	480
Pro	Leu	Ser	Gly	Lys	Cys	Gln	Leu	Ile	Trp	Cys	Ile	Asp	Pro	Val	Phe	
					150					155					160	
gcc	gcc	gag	ggc	acc	acc	agc	ccg	aac	acc	cgc	ctg	cta	gcg	gcc	acc	528
Ala	Ala	Glu	Gly	Thr	Thr	Ser	Pro	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Thr	
				165					170					175		
acc	gag	gaa	atg	acc	cgt	atg	ttc	ggc	gct	gac	cag	gca	ttt	tcc	cac	576
Thr	Glu	Glu	Met	Thr	Arg	Met	Phe	Gly	Ala	Asp	Gln	Ala	Phe	Ser	His	
			180					185					190			
cgg	ctg	agc	cgg	tgg	ccg	ctg	cat	gta	tct	gat	gat	ccg	acc	gcg	tac	624
Arg	Leu	Ser	Arg	Trp	Pro	Leu	His	Val	Ser	Asp	Asp	Pro	Thr	Ala	Tyr	
			195				200					205				
tcc	tgg	cac	tgc	cag	cac	aac	cga	gtc	gat	acg	ctt	gct	gag	ctg	atg	672
Ser	Trp	His	Cys	Gln	His	Asn	Arg	Val	Asp	Thr	Leu	Ala	Glu	Leu	Met	
						215					220					
gag	gta	gcc	cgc	acg	atg	acc	gga	tca	aaa	aag	cca	gat	agc	act	gct	720
Glu	Val	Ala	Arg	Thr	Met	Thr	Gly	Ser	Lys	Lys	Pro	Asp	Ser	Thr	Ala	
				230					235					240		
cac	cag	gag	ttt	tcc	agc	ggc	cgg	gca	cgg	atc	gaa	gcc	gcg	agg	aaa	768
His	Gln	Glu	Phe	Ser	Ser	Gly	Arg	Ala	Arg	Ile	Glu	Ala	Ala	Arg	Lys	
				245					250					255		
gcc	acc	gca	gaa	gcc	aaa	gcg	ctt	gct	gcc	tta	gac	gcc	acg	ctg	cct	816
Ala	Thr	Ala	Glu	Ala	Lys	Ala	Leu	Ala	Ala	Leu	Asp	Ala	Thr	Leu	Pro	
			260					265					270			
acg	gcg	ctg	gag	gca	tca	ggc	gat	ctc	att	gac	ggg	gtg	cgg	gtg	ctg	864
Thr	Ala	Leu	Glu	Ala	Ser	Gly	Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Leu	
			275				280					285				
tgg	gca	gca	gag	ggg	cgt	gca	gcc	cgt	gat	gag	acg	gcg	ttt	cgc	cat	912
Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His	
			290				295				300					
gcg	ttg	acc	gtg	ggg	tat	cag	ctt	aaa	gcc	gca	ggt	gaa	cgc	ctg	aaa	960
Ala	Leu	Thr	Val	Gly	Tyr	Gln	Leu	Lys	Ala	Ala	Gly	Glu	Arg	Leu	Lys	
				310					315				320			
gac	acc	aag	atc	att	gat	gcg	tat	gag	cgt	gcc	tac	aac	gtc	gcc	cag	1008
Asp	Thr	Lys	Ile	Ile	Asp	Ala	Tyr	Glu	Arg	Ala	Tyr	Asn	Val	Ala	Gln	
				325					330				335			
gcg	gtg	ggg	gct	gat	ggg	cgt	gag	ccg	gat	ctg	cct	gcc	atg	cgt	gat	1056
Ala	Val	Gly	Ala	Asp	Gly	Arg	Glu	Pro	Asp	Leu	Pro	Ala	Met	Arg	Asp	
				340				345					350			
cgt	cag	acg	ttg	gcc	cgt	cgt	gtg	cgc	gcc	tac	gtc	gct	aaa	ggc	cag	1104

Arg Gln Thr Leu Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln  
 355 360 365  
 ccc acg gtg agc gcc agg agc aca cag acc cag agc agc cgg ggc agg 1152  
 Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg  
 370 375 380  
 aaa gcc ctg gcc acc atg gga cgc aga ggc gca gcc acc tcg aat gca 1200  
 Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Ala Ala Thr Ser Asn Ala  
 385 390 395 400  
 cgc agg tgg gca gac cca gaa agc gat tac gcc cgc caa act cgg gag 1248  
 Arg Arg Trp Ala Asp Pro Glu Ser Asp Tyr Ala Arg Gln Thr Arg Glu  
 405 410 415  
 cgt tta gcc cga gca atg agc ttc gta cat tca gca cag acg aga aca 1296  
 Arg Leu Ala Arg Ala Met Ser Phe Val His Ser Ala Gln Thr Arg Thr  
 420 425 430  
 agg gcc gga tcc tgg cct acg ttt ccg agt gca agc gcc acg gtt acg 1344  
 Arg Ala Gly Ser Trp Pro Thr Phe Pro Ser Ala Ser Ala Thr Val Thr  
 435 440 445  
 acc cca cga gca aag aag tcg caa cgg agc tag 1377  
 Thr Pro Arg Ala Lys Lys Ser Gln Arg Ser  
 450 455

&lt;210&gt; 8

&lt;211&gt; 458

&lt;212&gt; PRT

<213> *Corynebacterium thermoaminogenes*

&lt;400&gt; 8

Met Thr Leu Ala Asp Ser Pro Gly Thr Tyr Thr Ala Asp Ala Trp Asn  
 1 5 10 15  
 Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser  
 20 25 30  
 Arg Gly Trp Asn His Gln Asp Ala Glu Phe Leu Ala His Leu Asp  
 35 40 45  
 Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp  
 50 55 60  
 Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val  
 65 70 75 80  
 Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro  
 85 90 95  
 Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln  
 100 105 110  
 Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu  
 115 120 125  
 Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn  
 130 135 140  
 Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe  
 145 150 155 160  
 Ala Ala Glu Gly Thr Thr Ser Pro Asn Thr Arg Leu Leu Ala Ala Thr  
 165 170 175  
 Thr Glu Glu Met Thr Arg Met Phe Gly Ala Asp Gln Ala Phe Ser His  
 180 185 190  
 Arg Leu Ser Arg Trp Pro Leu His Val Ser Asp Asp Pro Thr Ala Tyr  
 195 200 205  
 Ser Trp His Cys Gln His Asn Arg Val Asp Thr Leu Ala Glu Leu Met  
 210 215 220  
 Glu Val Ala Arg Thr Met Thr Gly Ser Lys Lys Pro Asp Ser Thr Ala

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<210> 9  
<211> 4369  
<212> DNA  
<213> *Corynebacterium thermoaminogenes*

<400> 9																
atg	act	cta	gcg	gat	tcg	cca	gga	aca	tac	aca	gca	gat	gcg	tgg	aat	48
Met	Thr	Leu	Ala	Asp	Ser	Pro	Gly	Thr	Tyr	Thr	Ala	Asp	Ala	Trp	Asn	
1				5					10					15		
tac	tcc	act	gat	ctg	ttc	gac	acc	cac	cct	gag	ctg	gct	tta	cgc	tcc	96
Tyr	Ser	Thr	Asp	Leu	Phe	Asp	Thr	His	Pro	Glu	Leu	Ala	Leu	Arg	Ser	
			20					25					30			
cgg	ggt	tgg	aat	cac	cag	gac	gcc	gca	gag	ttc	ctg	gcc	cac	ctg	gat	144
Arg	Gly	Trp	Asn	His	Gln	Asp	Ala	Ala	Glu	Phe	Leu	Ala	His	Leu	Asp	
		35					40					45				
cgc	agc	atg	ttt	cac	ggg	tgc	ccc	acc	cgg	gat	ttc	tcc	gcg	gcc	tgg	192
Arg	Ser	Met	Phe	His	Gly	Cys	Pro	Thr	Arg	Asp	Phe	Ser	Ala	Ala	Trp	
	50					55					60					
gtc	aaa	gac	ccg	gaa	acc	gga	gaa	acc	cgc	ccc	aag	ctg	cac	aga	gtt	240
Val	Lys	Asp	Pro	Glu	Thr	Gly	Glu	Thr	Arg	Pro	Lys	Leu	His	Arg	Val	
65				70					75					80		
ggc	acc	cgc	tca	ctt	tcc	cgg	tgc	cag	tac	gtt	gcc	ctg	acc	cac	ccg	288

Gly	Thr	Arg	Ser	Leu	Ser	Arg	Cys	Gln	Tyr	Val	Ala	Leu	Thr	His	Pro	
				85					90					95		
cag	cgc	tcc	gcg	gtg	ctg	gtc	tta	gac	atc	gac	atc	ccc	agc	cac	cag	336
Gln	Arg	Ser	Ala	Val	Leu	Val	Leu	Asp	Ile	Asp	Ile	Pro	Ser	His	Gln	
			100					105					110			
gcc	ggc	ggg	aac	atc	gag	cac	ctt	cac	ccg	cag	gtg	tac	gcc	acc	ttg	384
Ala	Gly	Gly	Asn	Ile	Glu	His	Leu	His	Pro	Gln	Val	Tyr	Ala	Thr	Leu	
			115				120					125				
gag	cgt	tgg	gca	cgg	gtg	gag	aaa	gcg	ccg	gcc	tgg	atc	ggg	gtg	aac	432
Glu	Arg	Trp	Ala	Arg	Val	Glu	Lys	Ala	Pro	Ala	Trp	Ile	Gly	Val	Asn	
			130				135				140					
ccg	ttg	tcg	gga	aag	tgc	cag	ctc	atc	tgg	tgc	att	gac	ccg	gtg	ttc	480
Pro	Leu	Ser	Gly	Lys	Cys	Gln	Leu	Ile	Trp	Cys	Ile	Asp	Pro	Val	Phe	
			145		150					155					160	
gcc	gcc	gag	ggc	acc	acc	agc	tcg	aac	acc	cgc	ctg	cta	gcg	gcc	acc	528
Ala	Ala	Glu	Gly	Thr	Ser	Ser	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Thr		
			165					170						175		
acc	gag	gaa	atg	acc	cgt	gtg	ttc	ggc	gct	gac	cag	gca	ttt	tcc	cac	576
Thr	Glu	Glu	Met	Thr	Arg	Val	Phe	Gly	Ala	Asp	Gln	Ala	Phe	Ser	His	
			180					185					190			
cgg	ctg	agc	cgg	tgg	ccg	ctg	cat	ggt	ttt	gat	gat	ccg	acc	gcg	tac	624
Arg	Leu	Ser	Arg	Trp	Pro	Leu	His	Val	Phe	Asp	Asp	Pro	Thr	Ala	Tyr	
			195				200					205				
tcc	tgg	cac	tgc	cag	cac	aac	cga	gtc	gat	att	ctt	gat	gag	ctg	atg	672
Ser	Trp	His	Cys	Gln	His	Asn	Arg	Val	Asp	Ile	Leu	Asp	Glu	Leu	Met	
			210			215					220					
gag	gta	gcc	cgc	acg	atg	acc	gga	tca	aaa	aag	ccg	aga	aag	cac	gct	720
Glu	Val	Ala	Arg	Thr	Met	Thr	Gly	Ser	Lys	Lys	Pro	Arg	Lys	His	Ala	
			225		230				235						240	
cac	cag	gag	ttt	tcc	agc	ggc	cgg	gca	cgg	atc	gaa	gcc	gcg	cgg	aaa	768
His	Gln	Glu	Phe	Ser	Ser	Gly	Arg	Ala	Arg	Ile	Glu	Ala	Ala	Arg	Lys	
			245					250						255		
gcc	acc	gca	gag	gcc	aaa	gcg	ctt	gcc	gcc	ttg	gac	gcc	acg	ctg	cct	816
Ala	Thr	Ala	Glu	Ala	Lys	Ala	Leu	Ala	Ala	Leu	Asp	Ala	Thr	Leu	Pro	
			260					265					270			
acg	gcg	ctg	gag	gca	tca	ggc	gat	ctc	att	gac	ggg	gtg	cgg	gtg	ttg	864
Thr	Ala	Leu	Glu	Ala	Ser	Gly	Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Leu	
			275				280					285				
tgg	gca	gca	gag	ggg	cgt	gca	gcc	cgt	gat	gag	aca	gcg	ttt	cgc	cat	912
Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His	
			290			295					300					
gcg	ttg	acc	gtg	ggt	tat	cag	ctt	aaa	gcc	gca	ggt	gaa	cgc	ctg	aaa	960
Ala	Leu	Thr	Val	Gly	Tyr	Gln	Leu	Lys	Ala	Ala	Gly	Glu	Arg	Leu	Lys	
			305		310				315					320		
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Asp	Ala	Lys	Ile	Ile	Asp	Ala	Tyr	Glu	Arg	Ala	Tyr	Asn	Val	Ala	Gln	
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Ala	Val	Gly	Ala	Asp	Gly	Arg	Glu	Pro	Asp	Leu	Pro	Ala	Met	Arg	Asp	
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Arg	Gln	Thr	Met	Ala	Arg	Arg	Val	Arg	Ala	Tyr	Val	Ala	Lys	Gly	Gln	
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